

**AMENDMENT**

Please amend the application, without prejudice, without admission, without surrender of subject matter, and without any intention of creating any estoppel as to equivalents, as follows:

**IN THE SPECIFICATION**

Please amend the paragraph beginning on page 8, line 13, as follows:

--The degree of homology is preferably determined by comparing the sequence of the respective nucleotide sequence with the coding region of SEQ ID No.1, particularly with region of SEQ ID No.1 (bp447-bp4607) which codes for the mature protein of the nucleotide sequence given in SEQ ID No. 1). If the sequences to be compared are of different lengths, the degree of homology preferably refers to the percentage of nucleotides in the shorter nucleotide sequence which are identical to the nucleotides of the longer sequence, i.e. the sequence identity is determined for the region in which the respective nucleotide sequences overlap. Sequence comparisons can be made using known computer programs, such as the ClustalW program (Thompson et al., Nucleic Acids Research 22, (1994), 4673-4680), which is distributed by Julie Thompson ([Thompson@EMBL-Heidelberg.DE](mailto:Thompson@EMBL-Heidelberg.DE)) and Toby Gibson ([Gibson@EMBL-Heidelberg.DE](mailto:Gibson@EMBL-Heidelberg.DE); European Molecular Biology Laboratory, Meyerhofstrasse 1, D 69117 Heidelberg, Germany). Clustal W can also be downloaded from various internet sites, e.g. that of the IGBMC (Institut de Génétique et de Biologie Moléculaire et Cellulaire, B.P.163, 67404 Illkirch Cedex, France; <ftp://ftp.igbmc.u-strasbg.fr/pub/>) and that of the EBI (European Bioinformatics Institute) (<ftp://ftp.ebi.ac.uk/pub/software/>), as well as from internet sites with links to the EBI (European Bioinformatics Institute, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SD, UK).--

Please amend the paragraph beginning on page 9, line 9, as follows:

--The degree of homology can be determined, for example, using known computer programs such as Mview (<http://www.sacbee.ucsf.edu/documentation/seqsoftware/mview>; Brown, N.P., Leroy C., Sander C. (1998). MView: A Web compatible database search or multiple alignment viewer. *Bioinformatics*, 14(4):380-381).--

Please delete the text of the specification entitled "Sequence protocol", beginning on page 48, line 5, and ending at the bottom of page 50 without prejudice.